Figure 1

Fatty Acid Biosynthetic Pathway

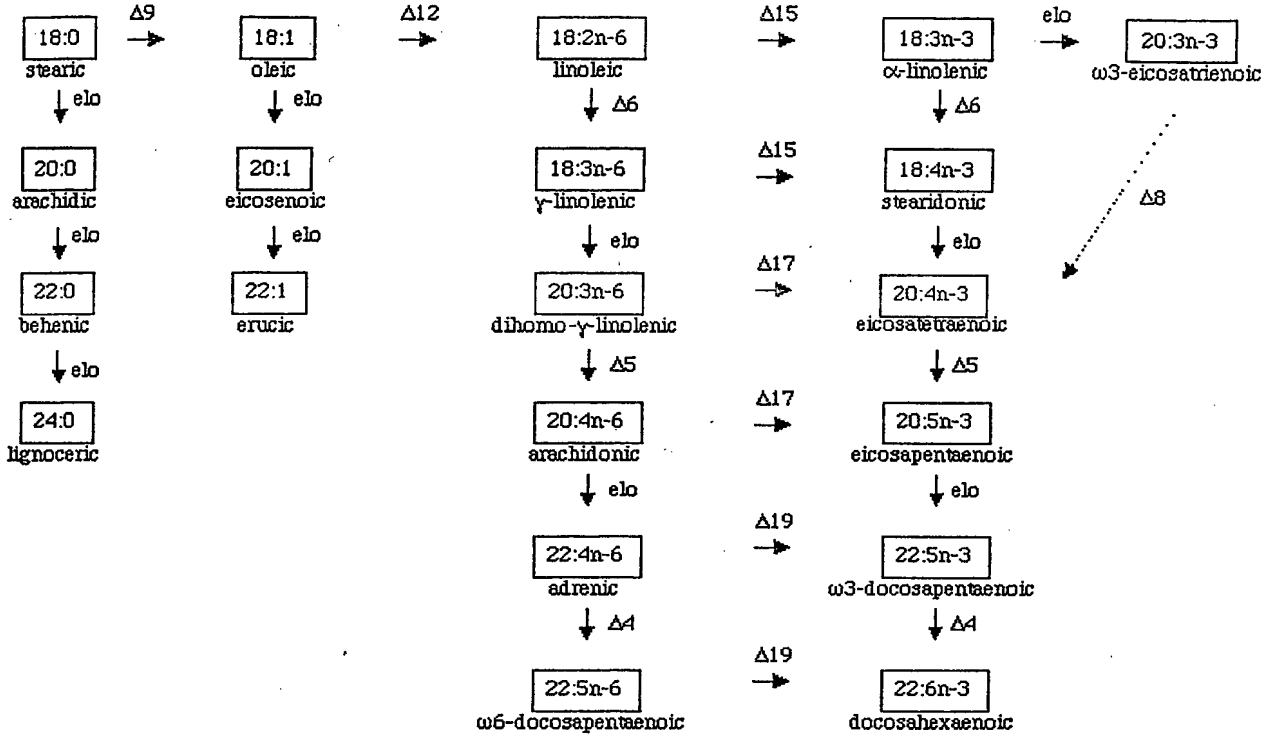

Figure 2

Gene Sequence of Delta 6- Desaturase from *Saprolegnia diclina* (ATCC 56851)

```
   1  ATGGTCCAGG GGCAAAAGGC CGAGAAGATC TCGTGGGCGA CCATCCGTGA
  51  GCACAACCGC CAAGACAACG CGTGGATCGT GATCCACCAC AAGGTGTACG
 101  ACATCTCGGC CTTTGAGGAC CACCCGGGCG GCGTCGTCAT GTTCACGCAG
 151  GCCGGCGAAG ACGCGACCGA TGCGTTCGCT GTCTTCCACC CGAGCTCGGC
 201  GCTCAAGCTC CTCGAGCAGT ACTACGTCGG CGACGTCGAC CAGTCGACGG
 251  CGGCCGTCGA CACGTCGATC TCGGACGAGG TCAAGAAGAG CCAGTCGGAC
 301  TTCATTGCGT CGTACCGCAA GCTGCGCCTT GAAGTCAAGC GCCTCGGCTT
 351  GTACGACTCG AGCAAGCTCT ACTACCTCTA CAAGTGCGCC TCGACGCTGA
 401  GCATTGCGCT TGTGTCGGCG GCCATTTGCC TCCACTTTGA CTCGACGGCC
 451  ATGTACATGG TCGCGGCTGT CATCCTTGGC CTCTTTTACC AGCAGTGCGG
 501  CTGGCTCGCC CATGACTTTC TGCACCACCA AGTGTTTGAG AACCACTTGT
 551  TTGGCGACCT CGTCGGCGTC ATGGTCGGCA ACCTCTGGCA GGGCTTCTCG
 601  GTGCAGTGGT GGAAGAACAA GCACAACACG CACCATGCGA TCCCCAACCT
 651  CCACGCGACG CCCGAGATCG CCTTCCACGG CGACCCGGAC ATTGACACGA
 701  TGCCGATTCT CGCGTGGTCG CTCAAGATGG CGCAGCACGC GGTCGACTCG
 751  CCCGTCGGGC TCTTCTTCAT GCGCTACCAA GCGTACCTGT ACTTTCCCAT
 801  CTTGCTCTTT GCGCGTATCT CGTGGGTGAT CCAGTCGGCC ATGTACGCCT
 851  TCTACAACGT TGGGCCCGGC GGCACCTTTG ACAAGGTCCA GTACCCGCTG
 901  CTCGAGCGCG CCGGCCTCCT CCTCTACTAC GGCTGGAACC TCGGCCTTGT
 951  GTACGCAGCC AACATGTCGC TGCTCCAAGC GGCTGCGTTC CTCTTTGTGA
1001  GCCAGGCGTC GTGCGGCCTC TTCCTCGCGA TGGTCTTTAG CGTCGGCCAC
1051  AACGGCATGG AGGTCTTTGA CAAGGACAGC AAGCCCGATT TTTGGAAGCT
1101  GCAAGTGCTC TCGACGCGCA ACGTGACGTC GTCGCTCTGG ATCGACTGGT
1151  TCATGGGCGG CCTCAACTAC CAGATCGACC ACCACTTGTT CCCGATGGTG
1201  CCCCGGCACA ACCTCCCGGC GCTCAACGTG CTCGTCAAGT CGCTCTGCAA
1251  GCAGTACGAC ATCCCATACC ACGAGACGGG CTTCATCGCG GGCATGGCCG
1301  AGGTCGTCGT GCACCTCGAG CGCATCTCGA TCGAGTTCTT CAAGGAGTTT
1351  CCCGCCATGT AA
```

Figure 3

Amino Acid Sequence of Delta 6- Desaturase from *Mortierella alpina* (ATCC 56851)

```
1     MVQGQKAEKI SWATIREHNR QDNAWIVIHH KVYDISAFED HPGGVVMFTQ
51    AGEDATDAFA VFHPSSALKL LEQYYVGDVD QSTAAVDTSI SDEVKKSQSD
101   FIASYRKLRL EVKRLGLYDS SKLYYLYKCA STLSIALVSA AICLHFDSTA
151   MYMVAAVIIG LFYQQCGWLA HDFLHHQVFE NHLEGDLVGV MVGNLMQGFS
201   VQWWKNKHNT HHAIPNLHAT PEIAFHGDPD IDTMPILAWS LKMAQHAVDS
251   PVGLFFMRYQ AYLYFPILLF ARISWVIQSA MYAFYNVGPG GTEDKVQYPL
301   LERAGLLLYY GWNLGLVYAA NMSLLQAAAF LFVSQASCGL FLAMVFSVGH
351   NGMEVFDKDS KPDFWKLQVL STRNVTSSLW IDWFMGGLNY QIDHHLFPMV
401   PRHNLPALNV LVKSLCKQYD IPYHETGFIA GMAEVVVHLE RISIEEFKEF
451   PAM*
```

Figure 4

Gene Sequence of Delta 5- Desaturase from *Saprolegnia diclina* (ATCC 56851)

```
   1  ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
  51  GCCGGTGGCC GGCAAGAAGG CCTTTACATG GCAGGAGGTC GCGCAGCACA
 101  ACACGGCGGC CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG
 151  ACCGAGTGGG CCAACAAGCA CCCCGGCGGC CGCGAGATGG TGCTGCTGCA
 201  CGCCGGTCGC GAGGCCACCG ACACGTTCGA CTCGTACCAC CCGTTCAGCG
 251  ACAAGGCCGA GTCGATCTTG AACAAGTATG AGATTGGCAC GTTCACGGGC
 301  CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
 351  CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG
 401  ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTTGC GGTCGCCGGC
 451  CTCGCCTTGT ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC
 501  GGCCGCGGCG CTCTTTGGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA
 551  TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCCATTAC
 601  GTCGTCGGCC GCTTTGCCAT GGACTGGTTT GCCGGCGGCT CGATGGTGTC
 651  ATGGCTCAAC CAGCACGTCG TGGGCCACCA CATCTACACG AACGTCGCGG
 701  GCTCGGACCC GGATCTTCCG GTCAACATGG ACGGCGACAT CCGCCGCATC
 751  GTGAACCGCC AGGTGTTCCA GCCCATGTAC GCATTCCAGC ACATCTACCT
 801  TCCGCCGCTC TATGGCGTGC TTGGCCTCAA GTTCCGCATC CAGGACTTCA
 851  CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
 901  GCGCTCTCGA CGTGGATGGC CATGATCAGC TCCAAGTCGT TCTGGGCCTT
 951  CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
1001  ACCTTGCGAT CTTCTTCCTC GCCGAGTTTG TCACGGGCTG GTACCTCGCG
1051  TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGCGGCT ACCCATGCGG
1101  CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA
1151  AGACGTCGGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC
1201  GGCGCGCTCA ACTACCAGGT CGTGCACCAC TTGTTCCCCA GCGTGTCGCA
1251  GTACCACTAC CCGGCGATCG CGCCCATCAT CGTCGACGTC TGCAAGGAGT
1301  ACAACATCAA GTACGCCATC TTGCCGGACT TTACGGCGGC GTTCGTTGCC
1351  CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT
1401  CCACATGGGC TAA
```

Figure 5

Amino Acid Sequence of Delta 5- Desaturase from *Saprolegnia diclina* (ATCC 56851)

1	MAPQTELRQR	HAAVAETPVA	GKKAFTWQEV	AQHNTAASAW	IIIRGKVYDV
51	TEWANKHPGG	REMVLLHAGR	EATDTFDSYH	PFSDKAESIL	NKYEIGTFTG
101	PSEFPTFKPD	TGFYKECRKR	VGEYFKKNNL	HPQDGFPGLW	RMMVVFAVAG
151	LALYGMHFST	IFALQLAAAA	LFGVCQALPL	LHVMHDSSHA	SYTNMPFFHY
201	VVGRFAMDWF	AGGSMVSWLN	QHVVGHHIYT	NVAGSDPDLP	VNMDGDIRRI
251	VNRQVFQPMY	AFQHIYLPPL	YGVLGLKFRI	QDFTDTFGSH	TNGPIRVNPH
301	ALSTWMAMIS	SKSFWAFYRV	YLPLAVLQMP	IKTYLAIFFL	AEFVTGWYLA
351	FNFQVSHVST	ECGYPCGDEA	KMALQDEWAV	SQVKTSVDYA	HGSWMTTFLA
401	GALNYQVVHH	LFPSVSQYHY	PAIAPIIVDV	CKEYNIKYAI	LPDFTAAFVA
451	HLKHLRNMGQ	QGIAATIHMG	*		

Figure 6

Gene Sequence of Delta 5- Desaturase from *Thraustochytrium aureum* (ATCC 34304)

```
1     ATGGGACGCG GCGGCGAAGG TCAGGTGAAC AGCGCGCAGG TGGCACAAGG
51    CGGTGCGGGA ACGCGAAAGA CGATCCTGAT CGAGGGCGAG GTCTACGATG
101   TCACCAACTT TAGGCACCCC GGCGGGTCGA TCATCAAGTT TCTCACGACC
151   GACGGCACCG AGGCTGTGGA CGCGACGAAC GCGTTTCGCG AGTTTCACTG
201   CCGGTCGGGC AAGGCGGAAA AGTACCTCAA GAGCCTGCCC AAGCTCGGCG
251   CGCCGAGCAA GATGAAGTTT GACGCCAAGG AGCAGGCCCG GCGCGACGCG
301   ATCACGCGAG ACTACGTCAA GCTGCGCGAG GAGATGGTGG CCGAGGGCCT
351   CTTCAAGCCC GCGCCCCTCC ACATTGTCTA CAGGTTTGCG GAGATCGCAG
401   CCCTGTTCGC GGCCTCGTTC TACCTGTTTT CGATGCGCGG AAACGTGTTC
451   GCCACGCTCG CGGCCATCGC AGTCGGGGGC ATCGCGCAGG GCCGCTGCGG
501   CTGGCTCATG CACGAGTGCG GACACTTCTC GATGACCGGG TACATCCCGC
551   TTGACGTGCG CCTGCAGGAG CTGGTGTACG GCGTGGGGTG CTCGATGTCG
501   GCGAGCTGGT GGCGCGTTCA GCACAACAAG CACCACGCGA CCCCGCAGAA
551   ACTCAAGCAC GACGTCGACC TCGACACCCT GCCGCTCGTT GCGTTCAACG
701   AGAAGATCGC CGCCAAGGTG CGCCCCGGCT CGTTCCAGGC CAAGTGGCTC
751   TCGGCGCAGG CGTACATTTT TGCGCCGGTG TCCTGCTTCC TGGTTGGTCT
301   CTTCTGGACC CTGTTTCTGC ACCCGCGCCA CATGCCGCGC ACGAGCCACT
351   TTGCTGAGAT GGCCGCCGTC GCGGTGCGCG TCGTGGGCTG GGCGGCGCTC
901   ATGCACTCGT TCGGGTACAG CGGGAGCGAC TCGTTCGGTC TCTACATGGC
951   CACCTTTGGC TTTGGCTGCA CCTACATCTT CACCAACTTT GCGGTCAGCC
1001  ACACGCACCT CGACGTCACC GAGCCGGACG AGTTCCTGCA CTGGGTCGAG
1051  TACGCCGCGC TGCACACGAC CAACGTGTCC AACGACTCGT GGTTCATCAC
1101  CTGGTGGATG TCGTACCTCA ACTTTCAGAT CGAGCACCAC CTCTTTCCGT
1151  CGCTGCCCCA GCTCAACGCC CCGCGCGTCG CCCCGCGCGT CCGCGCCCTC
1201  TTCGAGAAGC ACGGCATGGC TTACGACGAG CGCCCGTACC TTACCGCGCT
1251  TGGCGACACG TTTGCCAACC TGCACGCCGT GGGCCAAAAC GCGGGCCAGG
1301  CGGCGGCCAA GGCCGCTTAG
```

Figure 7

Amino Acid Sequence of Delta 5- Desaturase from *Thraustochytrium aureum* (ATCC 34304)

```
  1  MGRGGEGQVN SAQVAQGGAG TRKTILIEGE VYDVTNFRHP GGSIIKFLTT
 51  DGTEAVDATN AFREFHCRSG KAEKYLKSLP KLGAPSKMKF DAKEQARRDA
101  ITRDYVKLRE EMVAEGLFKP APLHIVYRFA EIAALFAASF YLFSMRGNVF
151  ATLAAIAVGG IAQGRCGWLM HECGHFSMTG YIPLDVRLQE LVYGVGCSMS
201  ASWWRVQHNK HHATPQKLKH DVDLDTLPLV AFNEKIAAKV RPGSFQAKWL
251  SAQAYIFAPV SCFLVGLFWT LFLHPRHMPR TSHFAEMAAV AVRVVGWAAL
301  MHSFGYSGSD SFGLYMATFG FGCTYIFTNF AVSHTHLDVT EPDEFLHWVE
351  YAALHTTNVS NDSWFITWWM SYLNFQIEHH LFPSLPQLNA PRVAPRVRAL
401  FEKHGMAYDE RPYLTALGDT FANLHAVGQN AGQAAAKAA
```

Figure 8

```
   1 GAATTCACCA TGGGTCGCGG AGCACAGGGA GAGCCAAGGC AGGCCACAGA
  51 GCTGAAGAGC AGCCCAAGTG AGCAGCGTAA GGTGTTGCTC ATTGACGGGC
 101 AGCTGTACGA TGCAACCAAC TTCAGGCATC CTGGTGGCTC CATCATCAAA
 151 TATTTGTGCA CCGATGGCAA GGAGGTAGTT GATGCAACCG AAGCGTACAA
 201 GGAGTTCCAC TGCAGATCCT CGAAGGCGGT CAAGTACCTC AACTCCCTGC
 251 CAAAGATCGA CGGCCCAATC AAGTACAAAT ACGACGCAAA GGAGCAGGCT
 301 CGCCATGACA AACTCACGAG GGAGTATGTA GCTCTCCGCG AACAGCTCGT
 351 CAAGGAGGGA TACTTTGACC CCAGCCCGCT CCACATTATC TACAGATGCG
 401 CCGAGTTGGC AGCCATGTTC GCTCTCTCGT TCTACCTTTT CTCCTTCAAG
 451 GGTAACGTCA TGGCCACTAT TGCTGCCATC GTGATTGGGG GGTGCGTGCA
 501 GGGTCGTTGT GGGTGGCTCA TGCATGAAGC TGGCCACTAC AGCATGACCG
 551 GAAACATCCC TGTTGACTTG CGCCTTCAAG AGTTTTTGTA CGGAATTGGG
 601 TGTGGCATGA GCGGGGCTTG GTGGAGAAGC CAGCACAACA AGCACCACGC
 651 CACCCCCCAA AAGCTCAAGC ATGACGTTGA TTTGGACACT CTTCCTCTTG
 701 TCGCCTGGAA CGAGAAAATT GCCCGTCGCG TCAAGCCAGG TAGCTTCCAG
 751 GCAAAGTGGC TTCATCTCCA GGGATACATC TTTGCCCCAG TCTCCTGCCT
 801 TCTCGTTGGT CTCTTCTGGA CTTTGTACTT GCATCCTCGC CACATGATCC
 851 GCACCAAGCG CAACTTCGAG ATATTTTCTG TCGCTCTGCG CTACGTATGC
 901 TGGTTCTCGC TTCTTTTGAG CATGGGCTAC ACTGTCGGAG AGTCTCTGGG
 951 TCTCTATGTG CTTACTTTTG GACTTGGCTG TACCTACATC TTTACGCATT
1001 TTGCTGTAAG CCACACCCAC TTGCCAGTGT CCGAGGAGGA CGAGTACCTG
1051 CACTGGGTCG AGTACGCTGC GCTGCACACC ACGAACGTTG CCATCGACTC
1101 GTACGTTGTC ACCTGGCTGA TGAGCTACCT CAACTTTCAG ATCGAGCACC
1151 ACTTGTTCCC TTGCTGCCCG CAGTTCCGCC ACCCTGCAAT CTCTTCTCGC
1201 GTCAAGAAAC TTTTCGAGGA CAATGGTCTG GTATACGACG CCCGCTCATA
1251 CGTCCAGGCG CTCAAGGATA CCTTCGGCAA CCTACACGAA GTGGGCGTCA
1301 ACGCTGGCCA AGCTGCCAAG AGCGAGTAAG ATCTCGAG
```

Start/stop underlined

Figure 9

```
  1  MGRGAQGEPR QATELKSSPS EQRKVLLIDG QLYDATNFRH PGGSIIKYLC
 51  TDGKEVVDAT EAYKEFHCRS SKAVKYLNSL PKIDGPIKYK YDAKEQARHD
101  KLTREYVALR EQLVKEGYFD PSPLHIIYRC AELAAMFALS FYLFSFKGNV
151  MATIAAIVIG GCVQGRCGWL MHEAGHYSMT GNIPVDLRLQ EFLYGIGCGM
201  SGAWWRSQHN KHHATPQKLK HDVDLDTLPL VAWNEKIARR VKPGSFQAKW
251  LHLQGYIFAP VSCLLVGLFW TLYLHPRHMI RTKRNFEIFS VALRYVCWFS
301  LLLSMGYTVG ESLGLYVLTF GLGCTYIFTH FAVSHTHLPV SEEDEYLHWV
351  EYAALHTTNV AIDSYVVTWL MSYLNFQIEH HLFPCCPQFR HPAISSRVKK
401  LFEDNGLVYD ARSYVQALKD TFGNLHEVGV NAGQAAKSE
```

Figure 10

```
   1  CCATGGGCCG CGGCGGCGAG AAAAGCGAGG TGGACCAGGT GCAGCCACAA
  51  AAGACCGAGC AGCTCCAGAA GGCCAAGTGG GAGGATGTTG TTCGCATCAA
 101  TGGAGTCGAA TACGACGTCA CGGACTATCT CAGAAAACAC CCTGGTGGCA
 151  GCGTGATCAA GTACGGGCTT GCCAACACCG GCGCTGATGC CACGTCCCTC
 201  TTTGAAGCGT TCCACATGCG CTCAAAGAAG GCTCAGATGG TGCTCAAGTC
 251  TCTCCCAAAG CGTGCTCCGG TCCTCGAGAT CCAGCCAAAC CAGCTTCCAG
 301  AGGAGCAGAC CAAGGAGGCG GAGATGCTGC GTGATTTTAA AAAATTTGAG
 351  GATGAGATTC GCCGGGATGG ATTGATGGAA CCTTCCTTCT GGCATCGCGC
 401  TTACAGATTA TCAGAGCTTG TAGGTATGTT CACGCTCGGC CTCTACCTCT
 451  TCTCGTTAAA CACTCCTCTG TCTATTGCTG CTGGTGTCCT CGTCCACGGT
 501  CTCTTTGGTG CATTCTGTGG ATGGTGCCAG CATGAGGCAG GCCACGGCTC
 551  CTTTTTTTAC AGCCTTTGGT GGGGCAAGCG TGTACAGGCC ATGTTGATCG
 601  GGTTTGGTCT AGGAACATCC GGCGACATGT GGAACATGAT GCACAACAAG
 651  CATCATGCTG CCACCCAAAA GGTTCATCAC GACCTTGACA TTGACACAAC
 701  TCCTTTTGTA GCTTTCTTCA ACACTGCATT TGAGAAAAAC AGATGGAAGG
 751  GCTTTTCCAA GGCTTGGGTC CGCTTTCAGG CTTTCACGTT CATTCCTGTC
 801  ACCAGCGGCA TGATCGTCAT GCTGTTCTGG CTGTTTTTTC TCCACCCTCG
 851  CCGCGTCGTT CAAAAGAAGA ACTTTGAGGA GGGTTTTTGG ATGCTGTCGA
 901  GCCACATTGT GCGCACCTAT CTCTTCCACC TTGTGACCGG CTGGGAGAGC
 951  CTCGCTGCAT GCTACCTTGT TGGGTATTGG GCGTGCATGT GGGTGTCCGG
1001  TATGTATTTG TTTGGCCACT TTTCGCTCTC CCACACTCAT ATGGACATTG
1051  TGGAGGCGGA CGTGCATAAG AACTGGGTCA GGTACGCTGT TGACCACACT
1101  GTTGACATCA GCCCATCCAA CCCGCTCGTG TGCTGGGTCA TGGGTTACCT
1151  CAACATGCAG ACCATCCACC ACTTGTGGCC TGCCATGCCC CAGTACCACC
1201  AGGTCGAGGT CTCACGCCGC TTTGCCATCT TCGCCAAAAA ACACGGCCTC
1251  AACTACCGCG TCGTCTCTTA CTTTGAGGCT TGGCGCCTGA TGCTCCAAAA
1301  TCTTGCTGAC GTCGGTTCCC ACTACCATGA GAACGGTGTC AAGCGCGCCC
1351  CAAAGAAAGC CAAGGCGCAG TAGAAAGCTA T
```

Start/stop underlined

Figure 11

```
  1 MGRGGEKSEV DQVQPQKTEQ LQKAKWEDVV RINGVEYDVT DYLRKHPGGS
 51  VIKYGLANTG ADATSLFEAF HMRSKKAQMV LKSLPKRAPV LEIQPNQLPE
101  EQTKEAEMLR DFKKFEDEIR RDGLMEPSFW HRAYRLSELV GMFTLGLYLF
151  SLNTPLSIAA GVLVHGLFGA FCGWCQHEAG HGSFFYSLWW GKRVQAMLIG
201  FGLGTSGDMW NMMHNKHHAA TQKVHHDLDI DTTPFVAFFN TAFEKNRWKG
251  FSKAWVRFQA FTFIPVTSGM IVMLFWLFFL HPRRVVQKKN FEEGFWMLSS
301  HIVRTYLFHL VTGWESLAAC YLVGYWACMW VSGMYLFGHF SLSHTHMDIV
351  EADVHKNWVR YAVDHTVDIS PSNPLVCWVM GYLNMQTIHH LWPAMPQYHQ
401  VEVSRRFAIF AKKHGLNYRV VSYFEAWRLM LQNLADVGSH YHENGVKRAP
451  KKAKAQ
```

Figure 12

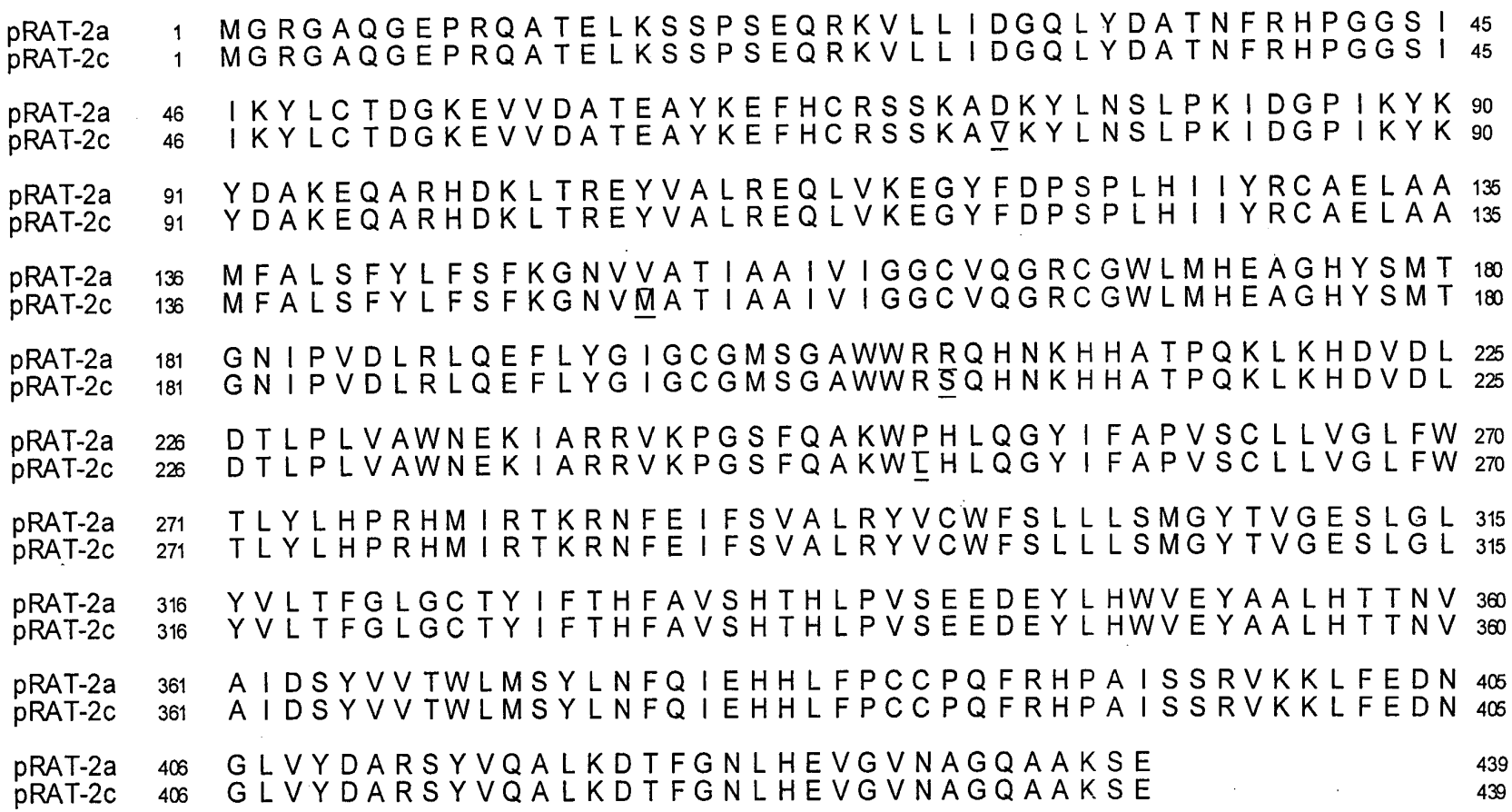

Figure 13

```
pRAT-1a    1  MGRGGEKSEVDQVQPQKTEQLQKAKWEDVVRINGVEYDVTDYLR  44
pRAT-1b    1  MGRGGEKSEVDQVQPQKTEQLQKAKWEDVVRINGVEYDVTDYLR  44

pRAT-1a   45  KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMVLKSLPKRA  88
pRAT-1b   45  KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMVLKSLPKRA  88

pRAT-1a   89  PVLEIQPNQLPEEQTKEAEMLRDFKKFEDEIRRDGLMEPSFWHR  132
pRAT-1b   89  PVLEIQPNQLPEEQTKEAEMLRDFKKFEDEIRRDGLMEPSFWHR  132

pRAT-1a  133  AYRLSELVGMFTLGLYLFSLNTPLSIAAGVLVHGLFGAFCGWCQ  176
pRAT-1b  133  AYRLSELVGMFTLGLYLFSLNTPLSIAAGVLVHGLFGAFCGWCQ  176

pRAT-1a  177  HEAGHGSFFYSLWWGKRVQAMLIGFGLGTSGDMWNMMHNKHHAA  220
pRAT-1b  177  HEAGHGSFFYSLWWGKRVQAMLIGFGLGTSGDMWNVMHNKHHAA  220

pRAT-1a  221  TQKVHHDLDIDTTPFVAFFNTAFEKNRWKGFSKAWVRFQAFTFI  264
pRAT-1b  221  TQKVHHDLDIDTTPFVAFFNTAFEKNRWKGFSKAWVRFQAFTFI  264

pRAT-1a  265  PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWMLSSHIVRTYLF  308
pRAT-1b  265  PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWMLSSHIVRTYLF  308

pRAT-1a  309  HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA  352
pRAT-1b  309  HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA  352

pRAT-1a  353  DVHKNWVRYAVDHTVDISPSNPLVCWVMGYLNMQTIHHLWPAMP  396
pRAT-1b  353  DVHKNWVRYAVDHTVDISPSNPLVCWVMGYLNMQTIHHLWPAMP  396

pRAT-1a  397  QYHQVEVSRRFAIFAKKHGLNYRVVSYFEAWRLMLQNLADVGSH  440
pRAT-1b  397  QYHQVEVSRRFAIFAKKHGLNYRVVSYFEAWRLMLQNLADVGSH  440

pRAT-1a  441  YHENGVKRAPKKAKAQ                              456
pRAT-1b  441  YHENGVKRAPKKAKAQ                              456
```

Figure 14

1 ATGGTGGCAG GCAAATCAGG CGCTGCGGCG CACGTGACTC ACAGCTCGAC
51 ATTGCCCCGT GAGTACCATG GCGCGACCAA CGACTCGCGC TCTGAGGCGG
101 CCGACGTCAC CGTCTCTAGC ATCGATGCTG AAAAGGAGAT GATCATCAAC
151 GGCCGCGTGT ATGACGTGTC GTCATTTGTG AAGCGGCACC CAGGTGGCTC
201 GGTGATCAAG TTCCAGCTGG GCGCCGACGC GAGCGACGCG TACAACAACT
251 TTCACGTCCG CTCCAAGAAG GCGGACAAGA TGCTGTATTC GCTCCCGTCC
301 CGGCCGGCCG AGGCCGGCTA CGCCCAGGAC GACATCTCCC GCGACTTTGA
351 GAAGCTGCGC CTCGAGCTGA AGGAGGAGGG CTACTTCGAG CCCAACCTGG
401 TGCACGTGAG CTACAGGTGT GTGGAGGTTC TTGCCATGTA CTGGGCTGGC
451 GTCCAGCTCA TCTGGTCCGG GTACTGGTTC CTCGGCGCGA TCGTGGCCGG
501 CATTGCGCAG GGCCGCTGCG GCTGGCTCCA GCATGAGGGT GGGCACTACT
551 CGCTCACCGG CAACATCAAG ATCGACCGGC ATCTGCAGAT GGCCATCTAT
601 GGGCTTGGCT GCGGCATGTC GGGCTGCTAC TGGCGCAACC AGCACAACAA
651 GCACCACGCC ACGCCGCAGA AGCTCGGGAC CGACCCCGAC CTGCAGACGA
701 TGCCGCTGGT GGCCTTCCAC AAGATCGTCG GCGCCAAGGC GCGAGGCAAG
751 GGCAAGGCGT GGCTGGCGTG GCAGGCGCCG CTCTTCTTTG GCGGGATCAT
801 CTGCTCGCTC GTCTCTTTCG GCTGGCAGTT CGTGCTCCAC CCCAACCACG
851 CGCTGCGCGT GCACAATCAC CTGGAGCTCG CGTACATGGG CCTGCGGTAC
901 GTGCTGTGGC ACCTGGCCTT TGGCCACCTC GGGCTGCTGA GCTCGCTCCG
951 CCTGTACGCC TTTTACGTGG CCGTGGGCGG CACCTACATC TTCACCAACT
1001 TCGCCGTCTC GCACACCCAC AAGGACGTCG TCCCGCCCAC CAAGCACATC
1051 TCGTGGGCAC TCTACTCGGC CAACCACACG ACCAACTGCT CCGACTCGCC
1101 CTTTGTCAAC TGGTGGATGG CCTACCTCAA CTTCCAGATC GAGCACCACC
1151 TCTTCCCGTC GATGCCGCAG TACAACCACC CCAAGATCGC CCCGCGGGTG
1201 CGCGCGCTCT TCGAGAAGCA CGGGGTCGAG TATGACGTCC GGCCATACCT
1251 GGAGTGTTTT CGGGTCACGT ACGTCAACCT GCTCGCCGTA GGCAACCCGG
1301 AGCACTCCTA CCACGAGCAC ACGCACTAG

Figure 15

```
1   MVAGKSGAAA HVTHSSTLPR EYHGATNDSR SEAADVTVSS IDAEKEMIIN
51  GRVYDVSSFV KRHPGGSVIK FQLGADASDA YNNFHVRSKK ADKMLYSLPS
101 RPAEAGYAQD DISRDFEKLR LELKEEGYFE PNLVHVSYRC VEVLAMYWAG
151 VQLIWSGYWF LGAIVAGIAQ GRCGWLQHEG GHYSLTGNIK IDRHLQMAIY
201 GLGCGMSGCY WRNQHNKHHA TPQKLGTDPD LQTMPLVAFH KIVGAKARGK
251 GKAWLAWQAP LFFGGIICSL VSFGWQFVLH PNHALRVHNH LELAYMGLRY
301 VLWHLAFGHL GLLSSLRLYA FYVAVGGTYI FTNFAVSHTH KDVVPPTKHI
351 SWALYSANHT TNCSDSPFVN WWMAYLNFQI EHHLFPSMPQ YNHPKIAPRV
401 RALFEKHGVE YDVRPYLECF RVTYVNLLAV GNPEHSYHEH TH
```